

identity among the three GSTs ranged from 50-59% and similarity ranged from 65-94%. All four of the sulfotransferases are type II transmembrane proteins with short cytoplasmic tails. There are three regions (region A, B and C) in which identities among the human GSTs range from 50-59% and similarities range from 65 to 94%. The amino acid sequence for the regions are:

A: (T/S)XRSGSSF(V/F)G(Q/E)LFXQX(P/L)(D/E)VF(F/Y)L(F/Y/M)EP(L/V/A)(W/Y)HV  
(SEQ ID NO: 33)

B: L(N/D)L(K/H)(V/I)(I/V)XLVRDPR(A/G)(V/I)(LAF) (SEQ ID NO: 34)

C: PXXL(Q/K)XXY(L/M)(L/V)VRYEDL(A/V)XXP (SEQ ID NO: 35)

*AI*  
*Cond*  

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Please replace the paragraph on page 57, starting on line 2 with the following paragraph:

*A2*  
For the RT-PCR analysis of the F2 mice, total RNA was purified from peripheral lymph nodes and mesenteric lymph nodes of HEC-GlcNAc6ST +/+ and -/- mouse by lysis and extraction with RNAZol (Tel-Test Inc, Friendwood, Texas). cDNA was synthesized from the total RNA using random hexamers for priming and AMV reverse transcriptase. PCR reactions were carried with the cDNAs and the following primers pairs:

KSGal6ST:

5' primer: 5'-AGTCATGTGGCCATCAAGACTGTGCGGGTG  
3' Primer: 5'-GGGAGATAAGGCAACAGTTAAAGACGGCCC  
(SEQ ID NOS: 10 & 11)

HEC-GlcNAc6ST:

5' primer: 5'-CATGGGTCAAGCATGCCTTCCATACTAACGCCA  
3' primer: 5'-CTCTGCTTGGGCTGAGGAGAAAGGGGCACTC  
(SEQ ID NOS: 12 & 13)

GlcNAc6ST:

5' primer: 5'-GCCTACCGCAAGGAGGTGTCGGACTGGTGGAC  
3' primer: 5'-ACTGTTAACCCGCTCATAGCCCAGCACGGCCAT  
(SEQ ID NOS: 14 & 15)

HPRT:

5' primer: 5'-CCTGCTGGATTACATCAAAGCACTG  
3' primer: 5'-TCCAACACTTCGTGGGTCCT  
(SEQ ID NOS: 16 & 17).